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Projecting environmental suitable areas for malaria transmission in China under climate change scenarios

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ABSTRACT

Introduction: The proportion of imported malaria cases in China has increased over recent years, and has presented challenges for the malaria elimination program in China. However, little is known about the geographic distribution and environmental suitability for malaria transmission under projected climate change scenarios.
Methods: Using the MaxEnt model based on malaria presence-only records, we produced environmental suitability maps and examined the relative contribution of topographic, demographic, and environmental risk factors for *P. vivax* and *P. falciparum* malaria in China.
Results: The MaxEnt model estimated that environmental suitability areas (ESAs) for malaria cover the central, south, southwest, east and northern regions, with a slightly wider range of ESAs extending to the northeast region for *P. falciparum*. There was spatial agreement between the location of imported cases and area environmentally suitable for malaria transmission. The ESAs of *P. vivax* and *P. falciparum* are projected to increase in some parts of southwest, south, central, north and northeast regions in the 2030 s, 2050 s, and 2080 s, by a greater amount for *P. falciparum* under the RCP8.5 scenario. Temperature and NDVI values were the most influential in defining the ESAs for *P. vivax*, and temperature and precipitation the most influential for *P. falciparum* malaria.
Conclusion: This study estimated that the ESA for malaria transmission in China will increase with climate change and highlights the potential establishment of further local transmission. This model should be used to support malaria control by targeting areas where interventions on malaria transmission need to be enhanced.

1. Introduction

Malaria, a mosquito-borne infectious disease caused by parasites of the genus *Plasmodium* is a significant public health problem in tropical and subtropical countries (WHO, 2013). In China, malaria has historically been a significant public health burden, reaching 30 million cases annually (Yin et al., 2013). However, several years of control effort have greatly decreased malaria transmission (Xia et al., 2014; Zhou et al., 2014). The nationwide Malaria Control Program initiated in 1955 (Tang, 2000; Yin et al., 2014) was consolidated at different times, including the formulation of the National Malaria Control Programme (NMCP) in 2006 (China Ministry of Health, 2012) and the National Malaria Elimination Programme (NMEP) in 2010 (China Ministry of Health, 2012). Because of investment in malaria control and technical assistance from experts in the field, the burden of malaria has been reduced substantially. The number of local malaria cases has sharply decreased and has been geographically confined (Feng et al., 2015; Zhang et al., 2014a, 2014b). Nevertheless, the proportion of imported malaria cases has been increasing over recent years, which has presented challenges for the malaria elimination program in China (L. Zhang. et al., 2014b; Zhou et al., 2016). This increase has been reported to be due to an increasing number of international travellers in association with growth of international investment, including in some malaria endemic countries (Lai et al., 2016; Liu et al., 2014). Africa and South East Asia are the main source regions for imported cases. (Song et al., 2016; Zhou et al., 2016). Available evidence also has shown a geographic expansion in the distribution of imported malaria cases, especially *P. falciparum* in China (Xia et al., 2014; Zhang et al., 2014a, 2014b). However, little evidence is available on the environmental suitability of areas in which local cases occur. This is despite the

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susceptibility of the malaria vectors in some areas of China to introduced malaria cases (Wang et al., 2015). For example, *An. Sinensis,* one of the four major *Anopheles* mosquitoes in China (*An. sinensis, An. minimus*, *An. dirus,* and *An. lesteri*) (Huang et al., 2015) were reported to be susceptible to imported *P. vivax* cases in some areas bordering Myanmar (Wang et al., 2015). This increases the possibility of the establishment of local transmission in previously non-endemic areas from imported malaria. Investigating the environmental suitability for establishment of malaria transmission is important in assisting strategic planning of malaria control.

Suitability of the environment determines the spatial and temporal distributions of infectious diseases. For vector borne-diseases such as malaria, environmental suitability relates to the factors required for survival and development of the transmitting vector, with climatic, topographical and land cover variables being among the best predictors identified by different studies (Ayala et al., 2009; Kulkarni et al., 2010). Remotely sensed land cover and Normalized Difference Vegetation Index (NDVI) were also important predictors of environmental suitability using Maximum Entropy Models (MaxEnt) (Foley et al., 2009; Kulkarni et al., 2010). Despite this, the relative importance of these factors in estimating future malaria risk has not been well investigated in many countries, including China.

The ecological requirements of malaria can be studied using the MaxEnt model relating disease occurrence data to a set of environmental variables (Guisan et al., 2005). The MaxEnt model, also known as the Ecological Niche Model (ENM) or Species Distribution Model (SDM) is a machine-learning algorithm to predict the geographic distribution of species on the basis of their known distribution (i.e. realized niche) in the environmental space. This model has been found to show better predictive ability than other related modelling approaches, such as GARP (Genetic Algorithm for Rule Set Production) (Phillips et al., 2006; Slater et al., 2012). The model is gaining increased attention because of its applicability, especially in a situation when absence data (zero cases) are not available. The MaxEnt model uses variables that are ecologically relevant to the species available in disease presence-only data and a random sample of available environmental conditions (a background sample) to quantity probability of presence (the environmental suitability index), thereby showing the locations where species are most likely to exist. A unique feature of this method is its ability to reduce model complexity by setting regularization – a process of introducing additional information (penalty) to prevent model over-fitting and hence improve the predictive performance of the model (Phillips et al., 2008). Studies conducted in Tanzania (Kulkarni et al., 2010) and Portugal (Capinha et al., 2009), found a high degree of spatial agreement between vector habitat and malaria distribution in human populations. It has been used widely in recent decades to estimate the geographic distribution of vector-borne disease such as cutaneous leishmaniasis (Chalghaf et al., 2016) and lymphatic filariasis (Slater et al., 2012). Other studies have used it to investigate environmental suitability for major malaria vectors and contributing factors (Kulkarni et al., 2010; Laporta et al., 2011; Obsomer et al., 2012), and to predict the likely range of habitats suitable for mosquitoes under changing global climate scenarios (McIntyre et al., 2017; Ren et al., 2016). One study conducted in China estimated an area suitable for *Anopheles* mosquitoes using bioclimatic and land use variables in the MaxEnt model (Ren et al., 2016). In this study we aim to assess environmental suitability of areas receptive to malaria transmission in China, and the relative contribution of environmental factors. Such findings have significant public health importance in guiding the strategies of disease control programs, by way of mapping areas to be targeted for surveillance and control.

2. Methods

2.1. Occurrence data and environmental layers

Malaria presence data for the period 2005–2014 were obtained from the China Information System for Disease Control and Prevention (CISDCP). A total of 933 *P. vivax* and 1449 *P. falciparum* locations were recorded to have imported malaria cases during the study period. Each observation was assigned a location by matching to geo-coordinates of the county. We selected five environmental variables frequently reported in the literature as determinants of malaria transmission. Meteorological variables (average temperature, rainfall and relative humidity) were available from China Climate Data Sharing Service Center (http://data.cma.cn/en/?r = data/index). Daily data recorded at all available weather stations in the country were averaged over the study period (2005–2014) to produce annual data. Kriging interpolation was applied to produce a raster map of meteorological variables at 10 km spatial resolution. Two other environmental variables: Normalized Difference Vegetation Index (NDVI) and elevation were included to assess the effect of vegetation coverage and topography on the transmission of malaria. Monthly NDVI values, from the USGS LP DAAC data (https://lpdaac.usgs.gov/dataset_discovery/modis/modis_products_table/myd13a3) at 1 km resolution were included as a surrogate of vegetation cover. Land cover and elevation data were available from the Global Land Cover Facility (www.landcover.org). Digital Elevation Model (DEM) for the whole country were available from the Consultative Group on International Agricultural Research-Consortium for Spatial Information (CGIAR-CSI) at 90 m resolution (http://srtm.csi.cgiar.org/). We maintained the consistency of spatial resolution among environment variables using the spatial re-sampling technique described in Ren et al. (2016). To produce more realistic resolution data, we used a bilinear re-sampling method for continuous variables and the nearest neighbourhood method for categorical variables in ArcGIS 10.3.1 (ESRI, 2014). In this way, all of the environmental variables (Table 1) were re-sampled to the largest cell size of all input datasets (10 × 10 km), and converted to ASCII format for use in MaxEnt Software (Merow et al., 2013). The shapefile of administrative boundaries was obtained from the DIVA-gis open access spatial database, and used

Table 1
Environmental variables used to develop the models for malaria in China.

Dataset	Description and source
Meteorological variables (Temperature, Rainfall, Relative humidity)	A continuous raster map of meteorological variables created through kriging interpolation of weather station based daily data accessed from China Climate Data Sharing Service Center (http://data.cma.cn/en/?r = data/index).
NDVI	Tiles of Normalized Difference Vegetation Indices (1 × 1 km resolution) accessed from USGS LP DAAC data (https://lpdaac.usgs.gov/dataset_discovery/modis/modis_products_table/myd13a3 overlay with area map, projected, mosaicked, and values extracted by mask.
Land cover	Gridded map of land cover classes obtained from the Global Land Cover Facility (www.landcover.org). Raster maps were extracted by mask (to the boundary map of China), re-sampled, and assigned to presence localities.
Elevation	The Digital Elevation Model (DEM) was accessed from the Consultative Group on International Agricultural Research-Consortium for Spatial Information (CGIAR-CSI) at 90 m resolution (http://srtm.csi. cgiar.org/). Continuous raster data were extracted by mask, re-sampled and assigned to presence localities.
Population	The interpolated county-level population of China was rasterized using kriging techniques.

NDVI = Normalized Difference Vegetation Index.

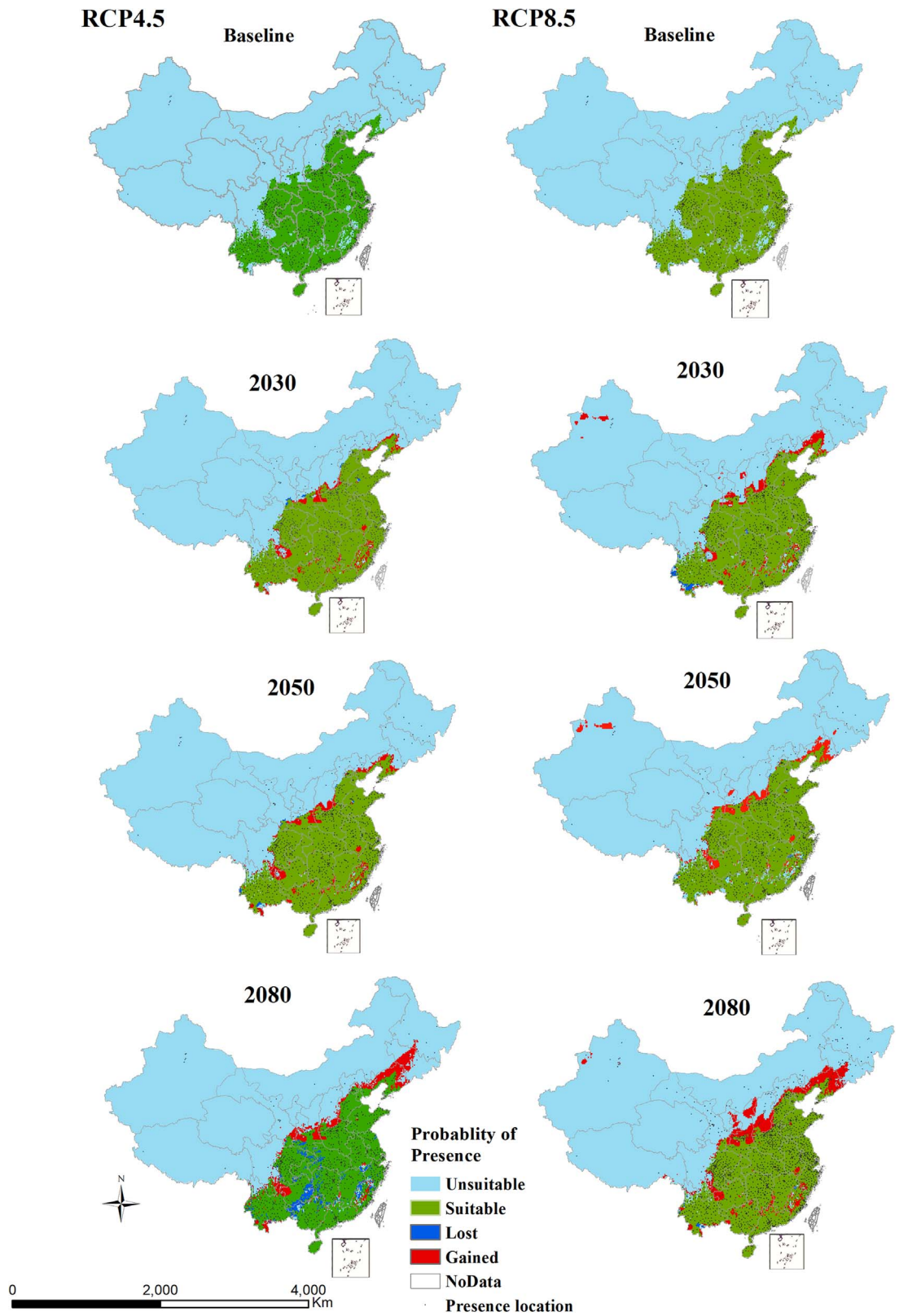

Fig. 1. Predicted distribution of baseline and future ESAs for *P. vivax* in China, under RCP4.5 and RCP8.5 climate scenarios. Green areas are predicted to be consistently suitable for malaria over time (prediction greater than or equal to the threshold); light blue areas are predicted to be consistently unsuitable. Dark blue areas are baseline ESAs which are predicted to become unsuitable for malaria; red areas are predicted to become suitable. Projections are based on ensembles of 26 global climate models (S Table 2). First and second columns show projections with RCP4.5 and RCP8.5, respectively. Black points indicate locations of imported malaria cases. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Table 2
Estimates of relative contributions of the environmental variables to the MaxEnt model.

Variables	Contribution (%) to *P. vivax* model	Contribution (%) to *P. falciparum* model
Temperature	45.1	40.0
Vegetation indices	28.5	6.7
Elevation	15.3	16.4
Population	6.1	14.7
Precipitation	0.9	21.7
Relative humidity	4.2	0.5

for mapping (Table 1).

2.2. Statistical analysis

We used the ecological niche model in MaxEnt software to predict environments potentially suitable for the occurrence of malaria in mainland China. Details of the method have been previously described (Merow et al., 2013; Phillips et al., 2006). Implementation of the model followed a standard protocol. Background pixel sampling, convergence thresholds, numbers of iterations and regularization, were specified according to the default rules of the software. Because the sampling process may bias presence data, especially in a study with large spatial coverage with a high proportion of less informative points we incorporated a sampling bias file in the MaxEnt's model settings as described in Chalghaf et al. (2016). The bias file weights background points according to their distance from the presence location, resulting in more reliable estimates (Phillips et al., 2008). In this way, we overcome the problems of sampling background points distant from historical sites of malaria occurrence, [http://www.sdmtoolbox.org/data/sdmtoolbox/current/User_Guide_SDMtoolbox_Chp5.pdf]. This method has also been reported to provide better predictive performance than random background sampling (Phillips et al., 2008).

In total, 1404 *P. vivax* and 745 *P. falciparum* presence locations were used for model development. For each malaria species, occurrence locations were randomly split into two sub-samples. Seventy-five percent of data were used as a training set to model the association between the occurrence of malaria and environmental variables, with the remaining twenty-five percent reserved for validation of the model outcome, as in previous studies (Kulkarni et al., 2010; Ren et al., 2016; Slater et al., 2012). We performed cross-validation with 10 replicate runs for each malaria type to take into account uncertainty introduced during the training and test splits. For the final prediction, we used all presence data in order to produce the best estimate of the malaria species distribution.

The performance of each model was evaluated using Area Under Curve (AUC) of the Receiver Operating Characteristic (ROC) (Kulkarni et al., 2010; Ren et al., 2016). This is a discriminatory measure that evaluates the capacity of the model to predict a higher probability of occurrence in the presence locations than un-sampled locations (M McPherson and Jetz, 2007) or probability that the occurrence location is predicted to have higher value than the random background site (pseudo-absence) (Suárez-Seoane et al., 2008), simulated (by default) in the MaxEnt software through random selection of background pixel (Phillips et al., 2006). A jackknife method was used to determine the relative contribution of the environmental variables. The MaxEnt model thus produces an AUC for all variables, as well as for omitting one variable at a time. Variables are ranked based on AUC values, higher values indicating greater influence. The relative contribution of each variable to the model was reported in percentage.

Cumulative probability was the output of the final model to obtain predicted ranges easily interpretable outputs (environmental suitability maps). A binary prediction of presence or absence was obtained using a "10 percentile training presence" threshold (corresponding to 10.40 for *P. vivax*, and 14.10 for the *P. falciparum*), as in previous studies (Phillips et al., 2006; Redon et al., 2010). This has been suggested as a better threshold value than more restricted thresholds because of its ecologically significant outcome (Redon et al., 2010). Threshold values were used to assign locations as suitable or unsuitable for *P. vivax* and *P. falciparum* malaria. Raster pixels in ASCII format were then imported into ArcGIS to produce the suitability map.

We estimated the impact of future climate (temperature and precipitation) on the ecology of malaria, based on an average of 26 global climate models (GCMs) under the recently developed representative concentration pathways (RCPs). The GCMs are representations of climate system processes including atmosphere, ocean, and cryosphere and land surface. GCMs are the main tools currently available for simulating the response of global climate to change in natural and anthropogenic radiative forcing (Climate Change, 2014). RCPs are scenarios adopted for use in climate change research to give a possible description of change in future climate with respect to anthropogenic greenhouse gasses concentration, air-pollutants, land use change and climate policies. We selected two scenarios representing medium stabilisation (RCP4.5) and high emission scenario RCP8.5 (Van Vuuren et al., 2011).

3. Results

Fig. 1 shows the estimated ESA for the two dominant malaria species in China. The average area under the curve (AUC) for *P. vivax and P. falciparum* models were 0.775 and 0.721, respectively (S Fig. 1). The AUC for all partitions of the presence data also showed that the MaxEnt model clearly discriminated between suitable and unsuitable environment for both malaria species (S Table 1).

Estimates of the relative contribution of environmental factors and elevation to model predictions of both malaria species are presented in Table 2. The results show that different variables contribute differently to the probability presence of *P. vivax* and *P. falciparum* malaria. Temperature and NDVI values were the most important variables for *P. vivax* malaria. For *P. falciparum*, the most important variables were temperature and precipitation. Although relative humidity affects vector and malaria distributions, the relative contribution of this climate factor was only 4.2% for *P. vivax* and 0.5% for *P. falciparum*. Elevation and population were other factors with a substantial contribution (Table 2).

3.1. ESA for malaria

The ESA of imported *P. vivax* and *P. falciparum* malaria cases is depicted in Figs. 1 and 2, respectively. The area currently suitable for *P. vivax* covers the southern, central parts of the south-western and northern regions, which are the most populated regions. Similarly, the ESA for *P. falciparum* covers the southwest to northeast with a wider distribution than for *P. vivax*. The majority of introduced malaria cases occurred in areas suitable for malaria transmission. For *P. falciparum*, about 1335 (92.1%) of the locations with *P. falciparum* cases were located within the area suitable for this species, and only 7.7% (n = 114) locations fell outside the estimated suitable areas. Similarly, 868 (93.0%) of the locations with imported *P. vivax* were within the area suitable for *P. vivax*, and 65 (6.9%) locations fell outside the suitable areas.

Compared to the baseline distribution the MaxEnt projection showed a consistent increase in environmentally suitable areas for *P. vivax* mostly along the edge of the baseline distribution in the south-western, central, east, north and northeast of China under both RCP4.5 and RCP8.5 scenarios in the 2030 s, and 2050 s and 2080 s. The projection also indicated an increase in the ESA in the 2030 s in some areas of the northwest China under RCP8.5 scenario. Although most current ESAs are predicted to remain suitable for *P. vivax* malaria under the climate scenarios explored, the ESA is projected to decrease substantially in some parts of central, south-western, and south of China in

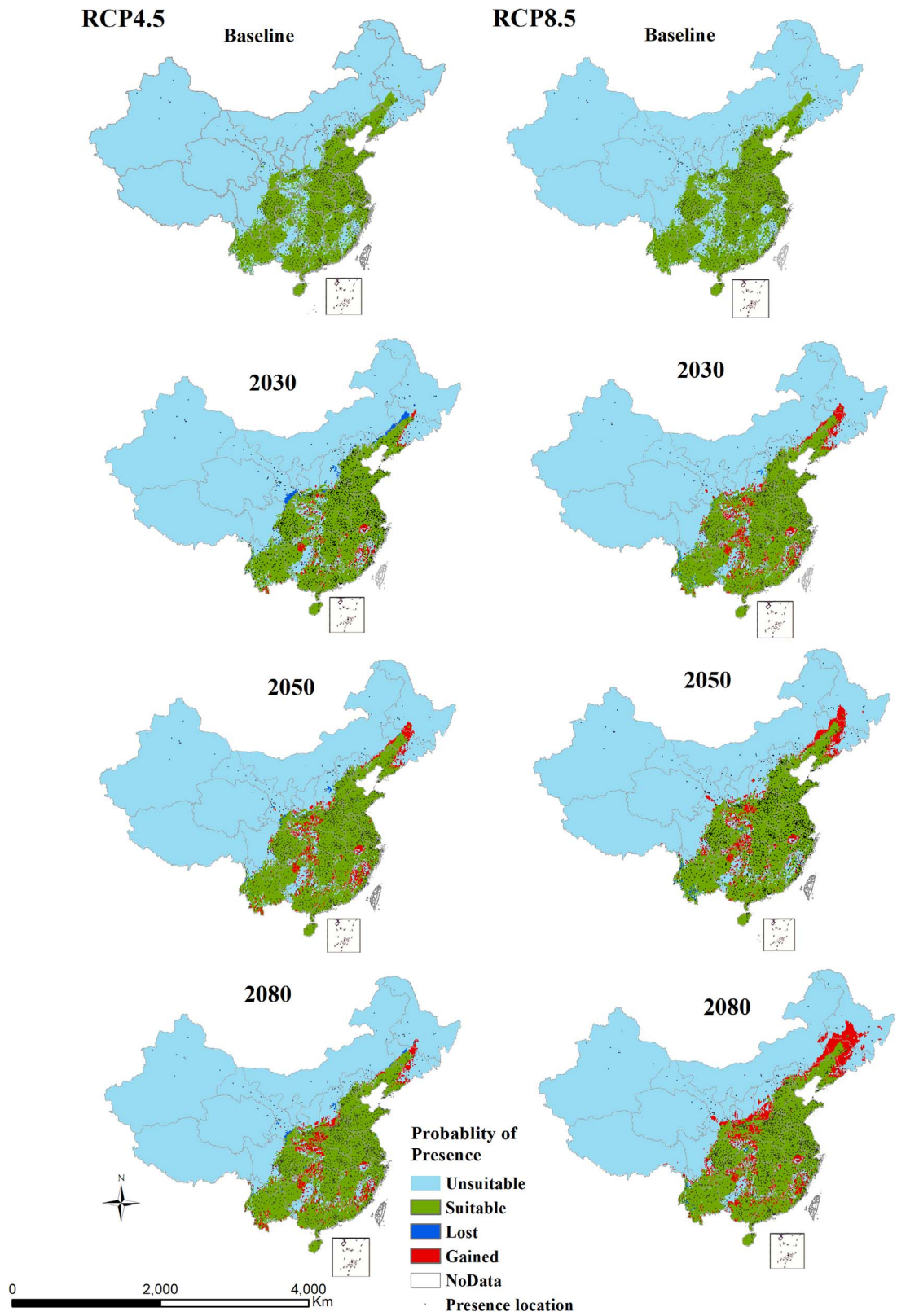

Fig. 2. Predicted distribution of baseline and future ESAs for *P. falciparum* in China, under RCP4.5 and RCP8.5 climate scenarios. Green areas are predicted to be consistently suitable for malaria over time (prediction greater than or equal to the threshold); light blue areas are predicted to be consistently unsuitable. Dark blue areas are baseline ESAs which are predicted to become unsuitable for malaria; red areas are projected to become suitable. Projections are based on ensembles of 26 global climate models (S Table 2). First and second columns show projections with RCP4.5 and RCP8.5, respectively. Black points indicate locations of imported malaria cases. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

the 2080 s under RCP4.5 (Fig. 1).

For *P. falciparum,* the ESA is projected to increase consistently in parts of southwest, southeast, south, central, north and northeast China in the 2030 s2030s, 2050 s, and 2080 s under both scenarios, and by a substantial amount under the RCP8.5 scenario. Conversely, the ESA of *P. falciparum* is projected to decrease in other parts of southwest, central, north and northeast China under RCP4.5 scenario (Fig. 2).

4. Discussion

We estimated the ESA for malaria transmission in mainland China, and identified the environmental determinants of this pattern using presence-only data in a species distribution model. Most imported malaria cases occurred in areas suitable for malaria. The model suggests that ESAs for *P. vivax* and *P. falciparum* are areas of endemic malaria transmission, with a wider range for *P. flaciparum* compared to *P. vivax*. The ESAs for both *P. vivax* and *P. falciparum* were predicted to be in parts of south, south-west, east, central and the north of China. However, the ESA for *P. falciparum* is projected to include some parts of the north-east. Temperature, elevation and vegetation indices contributed substantially to environmental suitability for the presence of malaria.

The ESA for both *P. vivax and P. falciparim* malaria included areas of endemic malaria transmission. Historically, malaria is endemic in the southern, south-western, eastern and central regions, and parts of the northern region of mainland China (Clements et al., 2009; Wen et al., 2011; Xia et al., 2015, 2014; Xiao et al., 2010; Yin et al., 2014; Zhang et al., 2008, 2012), presumably owing to their environmental suitability for malaria transmission (Gao et al., 2012; Huang et al., 2015). Previous studies have indicated that temperature, rainfall and relative humidity of these regions are suitable for malaria transmission (Hong et al., 2005). Distributions of the common malaria vectors have been found to be mainly concentrated in the south, southeast and central regions and some parts of southwest and north regions (Huang et al., 2015). Our findings also agree with those of a previous study using MaxEnt modelling of malaria vectors in China. Furthermore, all areas predicted to be suitable for malaria in this study include those previously predicted as suitable for *An. sinensis* (Ren et al., 2016). The geographic overlap of these areas with imported malaria cases highlights the need for circumvention of further local transmission. The government of China launched a malaria elimination program in 2010, working to eliminate the disease by 2020. Numbers of local malaria cases have greatly decreased, recently accounting for only 7% of total malaria reported in 2012 (Yin et al., 2013). The most recent evidence shows a substantial decline of malaria incidence in previously high endemic cross-border areas (Xu et al., 2016). This success has been driven by intensive malaria control interventions, including active case detection and management, vector control through the distribution of insect-side treated nets, indoor residual spraying and environmental improvement in high-transmission settings (Yin et al., 2014). Part of this success is the 1–3–7 strategy designed by the national malaria elimination in China to guide and monitor the malaria surveillance-response system. In this program, imported cases are investigated for the risk of establishing local transmission within 3 days. Malaria cases are then classified as active (i.e., local area is thought to support the malaria transmission), inactive (i.e., receptive areas have no potential for malaria transmission) or pseudo-active (if the area was previously non-endemic) based on the capacity of the local to support malaria transmission, with a response within 7 days. This strategy is well designed to enable prompt case detection and timely response. However, there are difficulties in implementation of this strategy (Lu et al., 2016; Zhou et al., 2015). Real-time surveillance and response must be realized, and cross-border collaboration with neighbouring endemic countries consolidated in response to imported malaria.

The majority of imported cases during the study period occurred in areas suitable for malaria transmission, indicating a high chance of local transmission of any imported malaria cases. However, secondary transmission is mainly determined by vectorial capacity and susceptibility of local malaria vectors to imported cases. *An. sinensis*, the most dominant malaria vector in China has low susceptibility to human host (Rueda et al., 2007) and vectorial capacity (Wang et al., 2015), related to host preference of the mosquito vector. Although this is widely reported in the literature (Wang et al., 2015), one recent study in malaria outbreak areas of central China reported an increased vectorial capacity of *An. sinsesis* for *P. vivax* malaria because of reduced livestock population (preferred host for the vector) associated with economic development and changes in the agricultural system (Pan et al., 2012b). Some local vectors were also found to be susceptible to imported *P. vivax* malaria cases in one county of Yunnan (Wang et al., 2015), pointing to the potential for establishing local transmission in this area. Vector control (indoor residual spraying and bed nets) has been actively implemented in southern China along the Myanmar border since the establishment of a National Malaria Elimination Program of China in 2010 (Wang et al., 2015). This and focused investigation conducted as part of the 1–3–7 strategy could further reduce the risk of local transmission.

Increase in the ESAs of *P. vivax* and *P. falciparum* toward the north and north-eastern regions of China are possibly related to predicted hotter and wetter climate in previously cooler regions (Chong-Hai et al., 2012; Tian et al., 2015), which could result in more areas becoming suitable for malaria transmission in the future.

The ESA for *P. falciparum* had a wider distribution than that for *P. vivax* malaria. This may be related to the increasing trend of imported malaria cases dominated by *P. falciparum* in recent years (Yin et al., 2013). Indeed, population movement itself is responsible for geographic expansion of malaria, especially *P. falciparum* in China. Using national malaria cases collected during 2004–2012, one study showed the number of counties with *P. falciparum* increased from 295 to 600 (Zhang et al., 2014a, 2014b). Increasing risk of imported *P. falciparum* malaria has been found to be mainly related to international travel (Song et al., 2016; Zhou et al., 2016). This can also be inferred from the patchy and extended distribution of *P. falciparum* localities observed in the present study. The difference in the geographic ranges of ESAs may indicate that the two malaria types respond differently to climatic factors (Casman et al., 2002; Gething et al., 2011; Grace An, 2011). One study reported that *P. falciparum* is more sensitive to climatic factors than *P. vivax* (Casman et al., 2002), and requires a narrower range of temperature than *P. vivax* to complete the entire process of its life cycle (Noden et al., 1995; Stratman-Thomas, 1940), and so may be more sensitive to changes in average temperature.

The present study showed the highest relative contribution of average temperature to the geographic distribution of malaria. The importance of optimum temperature as a determinant of malaria transmission stems from its indirect and direct effects on malaria vectors and malaria parasite maturation in the vector (Beck-Johnson et al., 2013; Gething et al., 2011). Similarly, our findings suggest that average temperatures could exercise the strongest effect on malaria presence. Vegetation also substantially influenced environmental suitability of malaria in the present study. The relationship between remote-sensed NDVI and malaria transmission has been previously reported (Ebhuoma et al., 2016). In our study, NDVI value spatially overlapped the distribution of malaria incidence in China (paper under review), likely due to some malaria vectors requiring shade for breeding sites. For example, *An. dirus,* and *An. minimus,* the main malaria vector in parts of Southeast Asia, prefer shaded breeding sites (Cameron et al., 2013). There is also a report on *An. dirus* complex found in forest and forest hills in some Southeast Asia countries (Obsomer et al., 2007). NDVI thus provides a measure of habitat suitability for malaria vectors. Precipitation also contributed to environmental suitability for transmission of malaria in this study. Rainfall governs malaria transmission by supporting the malaria vector (survival, development and density) and completion of the parasite life cycle (Reiter, 2001). While elevation played a role in

determining an ESA for malaria transmission in the present study, it appears its importance lies in its interaction with other environmental or meteorological factors. Indeed, elevation is closely associated with factors such as temperature, rainfall, vegetation and vector abundance. High altitude is characterized by high precipitation, low temperature and change in vegetation cover (Barry, 2012).

The present study has explored ecological correlates of malaria and used these to estimate environmentally suitable areas for malaria transmission across mainland China under present conditions and used recently projected climate scenarios to model future environmentally suitable areas. This is the first study to assess the potential effect of climate change on potential transmission of malaria for the 2030 s, 2050 s, and 2080 s in China. However, it should be noted that the resultant maps show the relative probability of presence rather than predicted number of malaria cases. Although environmental factors are determinants of malaria vectors rather than of the parasites, we used local malaria cases as a proxy for presence of malaria vectors as such are unavailable at national level. Distribution of malaria vectors might be impacted by factors other than the environmental factors we used. For example, malaria control interventions and pesticide application to agricultural fields in some areas of China may substantially reduce the density of *An. Antropopahagus* and therefore malaria incidence (Jiang et al., 2012a). Furthermore, we used a spatially coarse-scale (county level) malaria presence variables as outcome and predictor climatic variables (10 km × 10 km) as the spatial scale of the county. Possible changes in environmental factors across a year were also not considered. A dynamic modelling approach could combine these factors to obtain more detailed predictions. Overall, the study estimated an increase in the ESA for *P. vivax* and *P. falciparum* malaria species with climate change; and highlights the potential establishment of local transmission. MaxEnt modelling should support malaria control by targeting areas where the interventions on the disease transmission need to be enhanced.

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Conflict of interest

The authors report no conflict of interest.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.envres.2017.12.021

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